

## SEQUENCE LISTING

&lt;110&gt; SmithKline Beecham Biologicals S.A.

&lt;120&gt; Novel Compounds

&lt;130&gt; BM45412

&lt;160&gt; 10

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 1509

&lt;212&gt; DNA

<213> *Moraxella catarrhalis*

&lt;400&gt; 1

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cccgcctaaag	tggtggtaaa	aatggaaacc	gttgaaaaag	tcatgctgct	ggcagatggc	300
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&lt;210&gt; 2

&lt;211&gt; 502

&lt;212&gt; PRT

<213> *Moraxella catarrhalis*

&lt;400&gt; 2

Met	Ser	Lys	Pro	Thr	Leu	Ile	Lys	Thr	Thr	Leu	Ile	Cys	Ala	Leu	Ser
1				5				10				15			
Ala	Leu	Met	Leu	Ser	Gly	Cys	Ser	Asn	Gln	Ala	Asp	Lys	Ala	Ala	Gln
		20					25				30				
Pro	Lys	Ser	Ser	Thr	Val	Asp	Ala	Ala	Lys	Thr	Ala	Asn	Ala	Asp	

2

500

<210> 3  
 <211> 1506  
 <212> DNA  
 <213> *Moraxella catarrhalis*

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 gccgccaaga cagcaaatgc agataatgct gcctcacaag aacatcaagg cgagctgcct 180  
 gtcattgatg ccattgttac gcatgcacca gaagttccac cacctgttga ccgtgaccac 240  
 cccgccaag tggtggtaaa aatggaaacc gttgaaaaag tcatgctctt ggcagatggc 300  
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 gaaggcgaca ccatcgaagt gcagttctca aaccaccag attcaaaaat gccccataat 420  
 gttgactttc acgctgccac agggcctggc ggcggggcag aagcgtcatt taccgcaccg 480  
 ggtcatatat caacctttag ttttaaagcc ttacagcctg gtttgtatgt ctatcactgt 540  
 gcggttgccc ctggtggcat gcacattgct aatggcatgt atggtttgat tttggttgaa 600  
 ccaaaagagg gcttgccaaa agtagataaa gaatactatg tcatgcaagg cgacttttat 660  
 accaaaggca aatatggcga acaaggtcta cagccctttg atatggaaaa agccattcga 720  
 gaagatgctg aatatgttgt ctttaatggt tcggtggggg cgttgactgg tgaaaatgct 780  
 ctaaaagcca aggttgcgga aactgttcgc ttatttgttg gtaacggcgg ccggaatttg 840  
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 cacaacaaaa cagacgctgt ctatctgcca gaggggtgcc cacaagcaat tgatacccaa 1140  
 gaagcaccca aaacacctgc acctgccaac ttacaagagc agattaaagc aggtaaggca 1200  
 acctatgact ctaactgtgc tgcttgtcac caacctgatg gtaaaggcgt gccaaacgct 1260  
 ttcccaccgc ttgccaactc tgactatctg aacgccgacc acgctcgtgc cgccagcatc 1320  
 gtggcaaatg gattgtctgg taagattacc gtcaatggca accaatatga aagcgtcatg 1380  
 cctgcgattg ctctgagcga ccaacagatt gccaatgtca tcacctacac gcttaacagc 1440  
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 ccaaac 1506

<210> 4  
 <211> 502  
 <212> PRT  
 <213> *Moraxella catarrhalis*

<400> 4  
 Met Ser Lys Pro Thr Leu Ile Lys Thr Thr Leu Ile Cys Ala Leu Ser  
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 Ala Leu Met Leu Ser Gly Cys Ser Asn Gln Ala Asp Lys Ala Ala Gln  
 20 25 30  
 Pro Lys Ser Ser Thr Val Asp Ala Ala Lys Thr Ala Asn Ala Asp  
 35 40 45  
 Asn Ala Ala Ser Gln Glu His Gln Gly Glu Leu Pro Val Ile Asp Ala  
 50 55 60  
 Ile Val Thr His Ala Pro Glu Val Pro Pro Pro Val Asp Arg Asp His  
 65 70 75 80  
 Pro Ala Lys Val Val Val Lys Met Glu Thr Val Glu Lys Val Met Arg  
 85 90 95  
 Leu Ala Asp Gly Val Glu Tyr Gln Phe Trp Thr Phe Gly Gly Gln Val  
 100 105 110  
 Pro Gly Gln Met Ile Arg Val Arg Glu Gly Asp Thr Ile Glu Val Gln  
 115 120 125  
 Phe Ser Asn His Pro Asp Ser Lys Met Pro His Asn Val Asp Phe His

130	135	140
Ala Ala Thr Gly Pro Gly	Gly Gly Ala Glu Ala	Ser Phe Thr Ala Pro
145	150	155
Gly His Thr Ser Thr Ph	Ser Phe Lys Ala Leu	Gln Pro Gly Leu Tyr
165	170	175
Val Tyr His Cys Ala Val	Ala Pro Val Gly Met	His Ile Ala Asn Gly
180	185	190
Met Tyr Gly Leu Ile Leu	Val Glu Pro Lys Glu	Gly Leu Pro Lys Val
195	200	205
Asp Lys Glu Tyr Tyr Val	Met Gln Gly Asp Phe	Tyr Thr Lys Gly Lys
210	215	220
Tyr Gly Glu Gln Gly Leu	Gln Pro Phe Asp Met	Glu Lys Ala Ile Arg
225	230	235
Glu Asp Ala Glu Tyr Val	Val Phe Asn Gly Ser	Val Gly Ala Leu Thr
245	250	255
Gly Glu Asn Ala Leu Lys	Ala Lys Val Gly Glu	Thr Val Arg Leu Phe
260	265	270
Val Gly Asn Gly Gly Pro	Asn Leu Thr Ser Ser	Phe His Val Ile Gly
275	280	285
Glu Ile Phe Asp Lys Val	His Phe Glu Gly Gly	Lys Gly Glu Asn His
290	295	300
Asn Ile Gln Thr Thr Leu	Ile Pro Ala Gly Gly	Ala Ala Ile Thr Glu
305	310	315
Phe Lys Val Asp Val Pro	Gly Asp Tyr Val Leu	Val Asp His Ala Ile
325	330	335
Phe Arg Ala Phe Asn Lys	Gly Ala Leu Gly Ile	Leu Lys Val Glu Gly
340	345	350
Glu Glu Asn His Glu Ile	Tyr Ser His Lys Gln	Thr Asp Ala Val Tyr
355	360	365
Leu Pro Glu Gly Ala Pro	Gln Ala Ile Asp Thr	Gln Glu Ala Pro Lys
370	375	380
Thr Pro Ala Pro Ala Asn	Leu Gln Glu Gln Ile	Lys Ala Gly Lys Ala
385	390	395
Thr Tyr Asp Ser Asn Cys	Ala Ala Cys His Gln	Pro Asp Gly Lys Gly
405	410	415
Val Pro Asn Ala Phe Pro	Pro Leu Ala Asn Ser	Asp Tyr Leu Asn Ala
420	425	430
Asp His Ala Arg Ala Ala	Ser Ile Val Ala Asn	Gly Leu Ser Gly Lys
435	440	445
Ile Thr Val Asn Gly Asn	Gln Tyr Glu Ser Val	Met Pro Ala Ile Ala
450	455	460
Leu Ser Asp Gln Gln Ile	Ala Asn Val Ile Thr	Tyr Thr Leu Asn Ser
465	470	475
Phe Gly Asn Lys Gly Gly	Gln Leu Ser Ala Asp	Asp Val Ala Lys Ala
485	490	495
Lys Lys Thr Lys Pro Asn		
500		

<210> 5  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 5  
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WO 01/19996

PCT/EP00/09035

<210> 6  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 6  
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23

<210> 7  
<211> 17  
<212> DNA  
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<220>  
<223> primer

<400> 7  
gtaaaacgac ggccagt

17

<210> 8  
<211> 17  
<212> DNA  
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<220>  
<223> primer

<400> 8  
caggaaacag ctatgac

17

<210> 9  
<211> 22  
<212> DNA  
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<220>  
<223> primer

<400> 9  
acatgtctaa gcctactttg at

22

<210> 10  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 10  
agatctgttt ggcttggttt ttttggc

27